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OM protein - protein search, using sw model

Run on: December 20, 2004, 15:06:06 ; Search time 75 Seconds
(without alignments)
416.126 Million cell updates/sec

Title: US-10-670-911a-1

Perfect score: 480
Sequence: 1 AGKCDVAFGFSQCLKLDG.....RKESKNLTQSLFELCSG 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	100.0	87	Adm82927	Soluble c
2	480	100.0	142	AAW37859	Human neu
3	480	100.0	142	AAW37858	Rat neur
4	480	100.0	142	AAW37858	Human fet
5	480	100.0	142	AAW39848	Human pol
6	480	100.0	142	Adm63108	Rat Prote
7	480	100.0	142	Adm63114	Human Prote
8	480	100.0	142	Adm63112	Rat Prote
9	480	100.0	142	Adm63110	Human Prote
10	480	100.0	142	Adm04842	Antipso
11	480	100.0	142	AAW41634	Human pol
12	480	100.0	142	AAW89078	Polypepti
13	480	100.0	142	AAW89078	Human sec
14	480	100.0	142	AAW89078	Human sec
15	480	100.0	142	AAW89078	Human sec
16	480	100.0	142	AAW89078	Human sec
17	480	100.0	142	AAW89078	Human sec
18	480	100.0	142	AAW89078	Human sec
19	480	100.0	142	AAW89078	Human sec
20	480	100.0	142	AAW89078	Human sec
21	480	100.0	142	AAW89078	Human sec
22	480	100.0	142	AAW89078	Human sec
23	480	100.0	142	AAW89078	Human sec
24	480	100.0	142	AAW89078	Human sec
25	480	100.0	142	AAW89078	Human sec

26	179.5	37.4	165	4	AAW39830	Human pol
27	179.5	37.4	165	5	AAW3706	Human PRO
28	179.5	37.4	165	5	AAW6146	Human PRO
29	179.5	37.4	165	5	ABW84968	Human PRO
30	179.5	37.4	165	5	ABW85574	Human ang
31	179.5	37.4	165	6	ABW80853	Human PRO
32	179.5	37.4	165	6	ABW80853	Human PRO
33	179.5	37.4	165	6	ABW71438	Human neo
34	179.5	37.4	165	6	ABW82162	Novel hum
35	179.5	37.4	165	6	ABW72342	Human PRO
36	179.5	37.4	165	6	ABW72470	Human PRO
37	179.5	37.4	165	6	ABW34365	Human sec
38	179.5	37.4	165	7	ABW72172	Human mem
39	179.5	37.4	165	7	ABW83720	Human hum
40	179.5	37.4	165	7	ABW80826	Novel hum
41	179.5	37.4	165	7	ABW73367	Novel hum
42	179.5	37.4	165	7	ABW78449	Novel hum
43	179.5	37.4	165	7	ABW85097	Novel hum
44	179.5	37.4	165	7	ABW78203	Novel hum
45	179.5	37.4	165	7	ABW87269	Human PRO

ALIGNMENTS

RESULT 1
ADM82927 standard; protein; 87 AA.
XX
AC ADM82927;
XX
DT 01-JUL-2004 (first entry)
XX
DE Soluble candidate plasticity gene s-CPG15 core domain SEQ ID NO.1.
XX
KW cell death; soluble candidate plasticity gene; s-CPG15; CNS; cardiac;
XX gene therapy; Alzheimer's disease; Parkinson's disease;
XX Huntington's disease; amyotrophic lateral sclerosis;
XX traumatic brain injury; stroke; cardiac condition; cardiac ischemia;
XX s-CPG15 core domain.
XX
OS Homo sapiens.
XX
PN WO2004031347-A2.
XX
PD 15-APR-2004.
XX
PF 24-SEP-2003; 2003WO-US030152.
XX
PR 24-SEP-2002; 2002US-0413238P.
XX
PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX
PI Medivl E, Putz U;
XX
DR WPI; 2004-330162/30.
XX
PT Treating or preventing a condition of excessive cell death in a subject
PT comprising administering to the subject a soluble CPG15 (s-CPG15) compound
PT having s-CPG15 biological activity.
XX
PS Claim 5; SEQ ID NO 1; 92pp; English.
XX
The present invention describes a method for treating or preventing a
condition of excessive cell death in a subject, which comprises
administering to the subject a soluble candidate plasticity gene CPG15 (s-
CPG15) compound having s-CPG15 biological activity in an amount and for
a time sufficient to prevent, reduce, or eliminate the symptoms of the
condition. Also described: (1) a method of reducing or preventing cell
death by administering to a cell s-CPG15 in an amount and for a time to
reduce or prevent the cell death; (2) a method of promoting the survival
or differentiation of a cell by administering to the cell s-CPG15; (3) a
composition of matter comprising a purified polypeptide having s-CPG15

biological activity; (4) methods of treating or preventing a condition of undruggable cell survival in a subject; (5) methods of enhancing cell death; (6) a composition of matter comprising a purified antibody or antigen-binding fragment that specifically binds s-CPG15, or siRNA that is complementary to an mRNA sequence encoding s-CPG15; (7) a method of manufacturing s-CPG15 by expressing the s-CPG15 protein in a population of cells and isolating from the supernatant of the cell population the s-CPG15; and (8) a method of identifying a candidate compound that modulates cell death, cell survival, or cellular differentiation pathways. s-CPG15 has CNS and cardiac activities, and can be used in gene therapy. The methods are useful for treating or preventing Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, traumatic injury to the brain, or stroke, or a cardiac condition such as cardiac ischemia. The present sequence represents a specifically claimed s-CPG15 core domain amino acid sequence from the present invention.

Sequence 87 AA;

Query Match 100.0%; Score 480; DB 8; Length 87;
Best Local Similarity 100.0%; Pred. No. 7e-51;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGKCDVAFKGFSDCLLKGDSMANYPGGLDDKTNIKTVCTWEDFHSCTVTALTDCQEGA 60
1 AGKCDVAFKGFSDCLLKGDSMANYPGGLDDKTNIKTVCTWEDFHSCTVTALTDCQEGA 60

61 KDMWDLKRSKSNLNIQGSLELCGSG 87
61 KDMWDLKRSKSNLNIQGSLELCGSG 87

RESULT 2

AAW37859 standard; protein; 142 AA.

AAW37859;

10-AUG-1998 (first entry)

Human neuritin full length amino acid sequence.

Human neuritin; antibody; autonomic nervous system; Parkinson's disease;

CNS; peripheral nervous system; Alzheimer's disease; tissue implantation.

Homo sapiens.

MO9806843-A1.

19-FEB-1998.

07-AUG-1997; 97MO-US013949.

09-AUG-1996; 96US-00694579.

(AMGE-) AMGEN INC.

(YEDA) YEDA RES & DEV CO LTD.

Theill LE, Naeve GS;

WPI; 1998-159535/14.

N-PSDB; AAV29023.

New isolated neuritin gene - is used to develop products for treating e.g. Alzheimer's disease, Parkinson's disease, peripheral neuropathy and damaged or degenerated nervous system tissue.

Claim 1; Fig 4; 83pp; English.

This is the full length amino acid sequence of the human neuritin. The gene products (e.g. antibody, peptide fragments, etc) can be used to treat patients in whom various cells of the central, autonomic, or peripheral nervous system have been degenerated, as well as treatment of

e.g. Alzheimer's disease, Parkinson's disease. They can also be used in conjunction with surgical implantation of tissue in the treatment of diseases in which tissue implantation is indicated. The products can also be used for detection and diagnosis

Sequence 142 AA;

Query Match 100.0%; Score 480; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGKCDVAFKGFSDCLLKGDSMANYPGGLDDKTNIKTVCTWEDFHSCTVTALTDCQEGA 60
28 AGKCDVAFKGFSDCLLKGDSMANYPGGLDDKTNIKTVCTWEDFHSCTVTALTDCQEGA 87

61 KDMWDLKRSKSNLNIQGSLELCGSG 87
88 KDMWDLKRSKSNLNIQGSLELCGSG 114

RESULT 3

AAW37858 standard; protein; 142 AA.

AAW37858;

10-AUG-1998 (first entry)

Rat neuritin full length amino acid sequence.

Rat neuritin; antibody; autonomic nervous system; Parkinson's disease;

CNS; peripheral nervous system; Alzheimer's disease; tissue implantation.

Rattus sp.

MO9806843-A1.

19-FEB-1998.

07-AUG-1997; 97MO-US013949.

09-AUG-1996; 96US-00694579.

(AMGE-) AMGEN INC.

(YEDA) YEDA RES & DEV CO LTD.

Theill LE, Naeve GS;

WPI; 1998-159535/14.

N-PSDB; AAV29022.

New isolated neuritin gene - is used to develop products for treating e.g. Alzheimer's disease, Parkinson's disease, peripheral neuropathy and damaged or degenerated nervous system tissue.

Claim 1; Fig 3; 83pp; English.

This is the full length amino acid sequence of the rat neuritin. The gene products (e.g. antibody, peptide fragments etc) can be used to treat patients in whom various cells of the central, autonomic, or peripheral nervous system have been degenerated, as well as treatment of e.g. Alzheimer's disease, Parkinson's disease. They can also be used in conjunction with surgical implantation of tissue in the treatment of diseases in which tissue implantation is indicated. The products can also be used for detection and diagnosis

Sequence 142 AA;

Query Match 100.0%; Score 480; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGKCDVAFKGFSDCLLKGDSMANYPGGLDDKTNIKTVCTWEDFHSCTVTALTDCQEGA 60

DB 28 AAKCDVAFKGFSDCLLKLGDSVANYPGGLDDKTNIKTVCTYWEFHSCVTALTDCQEGA 87
 QY 61 KMMWDLRKESKNLNIQGSLEFELCGSG 87
 DB 88 KMMWDLRKESKNLNIQGSLEFELCGSG 114

RESULT 4

AA10235
 ID AAB10235 standard; protein: 142 AA.

XX AAB10235;

XX 16-NOV-2000 (first entry)

DE Human fetal brain protein fragment AS34_11.

XX Secreted protein; cytostatic; immunostimulatory; antimicrobial;

KW antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine;

KW cell proliferation; differentiation; regulator; treatment; tumor;

KW autoimmune disease; inflammatory disorder; wound; microbial infection;

XX viral disease; graft versus host reaction suppression.

XX Homo sapiens.

XX WO200037630-A1.

XX 29-JUN-2000.

XX 22-DEC-1999; 99WO-US031005.

XX 23-DEC-1998; 98US-00220876.

XX (GEMV) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR;

XX WPI; 2000-44261/38.

XX N-PSDB; AAA40501.

XX Secreted human proteins AS296-11 and AS34-11, useful for treating tumors,

PT autoimmune diseases, inflammatory disorders, wounds, microbial infections

XX and viral diseases.

XX Claim 9a; Page 209-210; 293pp; English.

XX This invention describes novel secreted human proteins (I) which have

CC cytostatic, immunostimulatory, antimicrobial, antiviral,

CC immunosuppressive, antiinflammatory and vulnerary activity and which act

CC as cytokine, cell proliferation or differentiation regulators. (I) is

CC useful for treating tumors, autoimmune diseases, inflammatory disorders,

CC wounds, microbial infections and viral diseases. (I) is also useful for

CC suppressing graft versus host reaction. AAB10226-B10288 represent the

CC secreted proteins encoded by AAA40490-AA40580 which are described in the

XX method of the invention

RESULT 5
 AAM39848
 ID AAM39848 standard; protein: 142 AA.
 XX AAM39848;
 XX 22-OCT-2001 (first entry)
 DE Human polypeptide SEQ ID NO 2993.

XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokine; thrombolytic; drug screening; arthritis; inflammation;

XX leukemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00486725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HISE-) HISEO INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa;

PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442853/47.

XX N-PSDB; AAI59004.

XX Novel nucleic acids and polypeptides, useful for treating disorders such

XX as central nervous system injuries.

XX Example 4; SEQ ID NO 2993; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the

XX encoded polypeptides (AAM8642-AAM42213) with nocotropic,

XX immunosuppressant and cytostatic activity. The polynucleotides are useful

XX in gene therapy. A composition containing a polypeptide or polynucleotide

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localized neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemia and

CC C.N.S disorders. Note: The sequence data for this patent did not form

XX part of the printed specification

XX Sequence 142 AA;

XX Query Match 100.0%; Score 480; DB 4; Length 142;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-50;

XX Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCDVAFKGFSDCLLKLGDSVANYPGGLDDKTNIKTVCTYWEFHSCVTALTDCQEGA 60

DB 28 AAKCDVAFKGFSDCLLKLGDSVANYPGGLDDKTNIKTVCTYWEFHSCVTALTDCQEGA 87

QY 61 KMMWDLRKESKNLNIQGSLEFELCGSG 87

DB 88 KMMWDLRKESKNLNIQGSLEFELCGSG 114

Db 28 AGKCDAVFKGFSDDLKLGDSMANYPGGLDDKTNIKVCTYWEDEPHSCVTYALTDCQEGA 87
Qy 61 KDMWDKLRKESKKNLNIQGSFELCGSG 87
Db 88 KDMWDKLRKESKKNLNIQGSFELCGSG 114

RESULT 6
ADE63108
ADE63108 standard; protein; 142 AA.

AC ADE63108;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein AAB53415, SEQ ID NO 9043.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI: 2003-268312/26.
XX GENBANK; AAB53415.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WFO at
CC ftp.wipo.int/pub/published_pct_sequences.

Seq Sequence 142 AA;
Query Match 100.0%; Score 480; DB 7; Length 142;
Best Local Similarity 100.0%; Pred. No. 1,3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 AGKCDAVFKGFSDDLKLGDSMANYPGGLDDKTNIKVCTYWEDEPHSCVTYALTDCQEGA 87
Qy 61 KDMWDKLRKESKKNLNIQGSFELCGSG 87
Db 88 KDMWDKLRKESKKNLNIQGSFELCGSG 114

RESULT 7
ADE63114
ADE63114 standard; protein; 142 AA.

AC ADE63114;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein NP_057672, SEQ ID NO 9049.
XX
XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI: 2003-268312/26.
XX GENBANK; NP_057672.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that

modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 142 AA:

Query Match 100.0%; Score 480; DB 7; Length 142;

Best Local Similarity 100.0%; Pred. No. 1.3e-50; Mismatches 0; Gaps 0;

Matches 87; Conservative 0; Indels 0; Gaps 0;

Db 1 AGKCDVAFKGFSDCLLKLDGSMANYPOGLDDKTNIKTVCTYMEDFHSCTVTALDCEGA 60

28 AGKCDVAFKGFSDCLLKLDGSMANYPOGLDDKTNIKTVCTYMEDFHSCTVTALDCEGA 87

61 KDMWDKLRKESKNLNIQGSLEFLCGSG 87

88 KDMWDKLRKESKNLNIQGSLEFLCGSG 114

RESULT 8

AD63112

ID ADE63112 standard; protein; 142 AA.

AC ADE63112;

DT 29-JAN-2004 (first entry)

DE Rat Protein AAB53415, SEQ ID NO 9047.

KW Rat, pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus;

PN MO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

PT WPI; 2003-268312/26.

DR GENBANK; AAB53415.

XX

XX

XX

XX

XX

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially

expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 142 AA:

Query Match 100.0%; Score 480; DB 7; Length 142;

Best Local Similarity 100.0%; Pred. No. 1.3e-50; Mismatches 0; Gaps 0;

Matches 87; Conservative 0; Indels 0; Gaps 0;

Db 1 AGKCDVAFKGFSDCLLKLDGSMANYPOGLDDKTNIKTVCTYMEDFHSCTVTALDCEGA 60

28 AGKCDVAFKGFSDCLLKLDGSMANYPOGLDDKTNIKTVCTYMEDFHSCTVTALDCEGA 87

61 KDMWDKLRKESKNLNIQGSLEFLCGSG 87

88 KDMWDKLRKESKNLNIQGSLEFLCGSG 114

RESULT 9

AD63110

ID ADE63110 standard; protein; 142 AA.

AC ADE63110;

DT 29-JAN-2004 (first entry)

DE Human Protein NP_057672, SEQ ID NO 9045.

KW Human, pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN MO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

PT WPI; 2003-268312/26.

DR GENBANK; NP_057672.

XX

XX

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 142 AA:

Query Match 100.0%; Score 480; DB 7; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGKCDVAFKGFSPDCLTKLGDGMVNYPGGLDDKTNIKVCTYWEDEPHSCVTALTDCQEGA 60
28 AGKCDVAFKGFSPDCLTKLGDGMVNYPGGLDDKTNIKVCTYWEDEPHSCVTALTDCQEGA 87
61 KDMWDKLRKESKNLNIQGSFLFELCGSG 87
88 KDMWDKLRKESKNLNIQGSFLFELCGSG 114

RESULT 10

ADN04842

ADN04842 standard; protein; 142 AA.

ADN04842; (first entry)

Antipsoriatic protein sequence #601.

antipsoriatic; gene therapy; psoriasis; diagnosis.

Homo sapiens.

MO2004028479-A2.

08-APR-2004.

25-SEP-2003; 2003WO-US030907.

25-SEP-2002; 2002US-0414006P.

(GENTH) GENENTECH INC.

Rodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

WU TD;

WPI: 2004-305105/28.

N-PSDB; ADN04841.

New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in a

PT mammal.
XX
PS Claim 9; SEQ ID NO 1236; 3069bp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

SQ Sequence 142 AA:

Query Match 100.0%; Score 480; DB 8; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGKCDVAFKGFSPDCLTKLGDGMVNYPGGLDDKTNIKVCTYWEDEPHSCVTALTDCQEGA 60
28 AGKCDVAFKGFSPDCLTKLGDGMVNYPGGLDDKTNIKVCTYWEDEPHSCVTALTDCQEGA 87
61 KDMWDKLRKESKNLNIQGSFLFELCGSG 87
88 KDMWDKLRKESKNLNIQGSFLFELCGSG 114

RESULT 11

AAW41634

AAW41634 standard; protein; 154 AA.

AAW41634; (first entry)

Human polypeptide SEQ ID NO 6565.

Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

Homo sapiens.

MO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US034263.

23-DEC-1999; 99US-00471275.

21-JAN-2000; 2000US-00488725.

25-APR-2000; 2000US-00552317.

20-JUN-2000; 2000US-00598042.

19-JUL-2000; 2000US-00620312.

03-AUG-2000; 2000US-00653450.

14-SEP-2000; 2000US-00662191.

19-OCT-2000; 2000US-00693036.

29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

Zhou P, Goodrich R, Drmanac R;

WPI: 2001-442253/47.

N-PSDB; AAI60790.

Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.

Example 2; SEQ ID NO 6565; 10078bp; English.

PT disorders, immune diseases, inflammation or blood disorders.
 XX
 PS Disclosure; Page 149; 772pp; English.
 XX
 CC The invention relates to nucleic acid sequences (AAV4411 to AAV4613)
 CC encoding human secreted proteins (AAV48534 to AAV48756). The secreted
 CC protein gene sequences are deposited with the ATCC under deposit numbers
 CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
 CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
 CC cells comprising recombinant vectors containing the nucleic acid
 CC sequences are used for the recombinant production of the secreted
 CC proteins. The polynucleotide and amino acid sequences are useful for are
 CC useful for preventing, treating or ameliorating medical conditions e.g.
 CC by protein or gene therapy. Pathological conditions can be also diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the polynucleotides, based on
 CC which tissues they are most highly expressed in, and include developing
 CC products for the diagnosis or treatment of cancer, neurodegenerative
 CC disorders, developmental abnormalities and foetal deficiencies, blood
 CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
 CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
 CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
 CC osteoporosis, prostate diseases, obesity, disorders involving osteoclasts
 CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung
 CC or thymus, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners. The
 CC present sequence represents a polypeptide fragment encoded by a gene of
 CC the invention (see descriptor line for gene number).
 XX
 SO Sequence 143 AA;
 Query Match 88.9%; Score 426.5; DB 2; Length 143;
 Best Local Similarity 90.9%; Pred. No. 5e-44; 7; Indels 1; Gaps 1;
 Matches 80; Conservative 0; Mismatches 7;
 DB 1 AGKCDVAFKGFSDCLIKLGDG-MANYPQGLDDKTNITKVTCTWEDFHSCTVATLDCQSG 59
 DB 28 AGKCDVAFKGFSDCLIKLGDGXXXXXXPAAMDCKTNITKVTCTWEDFHSCTVATLDCQSG 87
 QY 60 AKDMMWDLKRSKKNLTQGSLEFCGSG 87
 DB 88 AKDMMWDLKRSKKNLTQGSLEFCGSG 115
 XX
 RESULT 13
 ABB51249
 ABB51249 standard; protein: 143 AA.
 XX
 ABB51249;
 DT 07-FEB-2002 (first entry)
 XX
 DE Human secreted protein encoded by gene 192 SEQ ID NO:1202.
 XX
 KM Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
 KM dermatologic; immunosuppressive; anti-inflammatory; immunostimulant;
 KM cytoskeletal; cardiac; anti-angiogenic; ophthalmological;
 KM neuroprotective; neurotrophic; anticonvulsant; antialzheimer's; vulnary;
 KM antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
 KM multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
 KM human immunodeficiency virus; hyperproliferative disorder; wound healing;
 KM Gaucher's disease; cardiovascular disease; Simillar syndrome; chemotaxis;
 KM Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
 KM corneal graft neovascularisation; diabetic retinopathy; regeneration;
 KM neurological disorder; Huntington's chorea; Alzheimer's disease;
 KM Parkinson's disease; infectious disease; chromosome 6.
 XX
 OS Homo sapiens.
 XX
 XX MO200162891-A2.
 XX
 XX 30-AUG-2001.

XX
 PF 21-FEB-2001; 2001WO-US005614.
 XX
 PR 24-FEB-2000; 2000US-0184836P.
 PR 29-MAR-2000; 2000US-0193170P.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA,
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y,
 PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferris AM, Fan P,
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, Zeng Z,
 PI Greene JM;
 XX
 DR WPI; 2001-625724/72.
 XX
 PT Nucleic acids encoding 207 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease
 PT and diabetic retinopathy.
 XX
 PS Disclosure; Page 414; 1533pp; English.
 XX
 CC ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
 CC activities based on the tissues and cells the genes are expressed in.
 CC Example of these activities include: immunomodulatory; antisclerotic;
 CC dermatologic; immunosuppressive; anti-inflammatory; immunostimulant;
 CC anti-HIV; cytoskeletal; cardiac; anti-angiogenic; ophthalmological;
 CC neuroprotective; neurotrophic; anticonvulsant; antialzheimer's; vascular;
 CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Schmitt's syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83195 to
 CC ABA83193 and ABB50300 represent sequences used in the exemplification of
 CC the present invention
 XX
 SO Sequence 143 AA;
 Query Match 88.9%; Score 426.5; DB 4; Length 143;
 Best Local Similarity 90.9%; Pred. No. 5e-44; 7; Indels 1; Gaps 1;
 Matches 80; Conservative 0; Mismatches 7;
 DB 1 AGKCDVAFKGFSDCLIKLGDG-MANYPQGLDDKTNITKVTCTWEDFHSCTVATLDCQSG 59
 DB 28 AGKCDVAFKGFSDCLIKLGDGXXXXXXPAAMDCKTNITKVTCTWEDFHSCTVATLDCQSG 87
 QY 60 AKDMMWDLKRSKKNLTQGSLEFCGSG 87
 DB 88 AKDMMWDLKRSKKNLTQGSLEFCGSG 115
 XX
 RESULT 14
 ABO45506
 ABO45506 standard; protein: 143 AA.
 XX
 AC ABO45506;
 XX
 DT 03-OCT-2003 (first entry)
 XX
 DE Novel human secreted protein #192 fragment #6.
 XX
 KM Human; gene therapy; autoimmune disorder; multiple sclerosis; cancer;
 KM systemic lupus erythematosus; haematopoietic cell disorder; allergy;
 KM agammaglobulinaemia; ataxia telangiectasia; blood coagulation disorder;
 KM afibrinogenaemia; thrombocytopenia; graft-versus-host disease; arthritis;
 KM inflammatory condition; ischaemia-reperfusion injury; infectious disease;

KM Hyperproliferative disorder; purpura; viral infection; regeneration;
 KM Bacterial infection; ulcer; Alzheimer's disease.
 XX Homo sapiens.
 OS US2003065160-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 07-DEC-2001; 2001US-00004860.
 XX
 PR 06-JUN-1997; 97US-0048875P.
 PR 06-JUN-1997; 97US-0048876P.
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 PR 05-SEP-1997; 97US-0057961P.
 PR 05-SEP-1997; 97US-0057962P.
 PR 05-SEP-1997; 97US-0057963P.

PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Young P, Greene JM, Perrie AM, Ruben SM, Rosen CA, Hu J;
 PI Olsen HS, Ebner R, Brewet LA, Moore PA, Shi Y, Florence C;
 PI Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
 PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
 PI Carter KC;
 XX
 DR WPI; 2003-540804/51.
 XX
 PT New isolated protein, useful for preparing a composition for diagnosing
 PT or creating cancer, inflammatory, immune or infectious diseases.
 XX
 PS Disclosure; Page 117; 172pp; English.
 XX
 CC The invention relates to an isolated HEMAB80 protein. The protein is
 CC useful for preparing a composition for diagnosing or treating autoimmune
 CC disorders e.g. multiple sclerosis and systemic lupus erythematosus;
 CC haematopoietic cell disorders e.g. agammaglobulinemia and ataxia
 CC telangiectasia; blood coagulation disorders e.g. fibrinogenemia and
 CC thrombocytopenia; allergy; graft-versus-host disease; inflammatory
 CC conditions e.g. ischaemia-reperfusion injury and arthritis;
 CC hyperproliferative disorders e.g. cancer and purpura; infectious disease
 CC e.g. viral infection and bacterial infection. The polynucleotide or
 CC protein can be used to regenerate damaged tissue e.g. ulcers and
 CC Alzheimer's disease. The present sequence represents the amino acid
 CC sequence of a novel human secreted protein fragment. Note: The sequence
 CC data for this patent did not form part of the printed specification but
 CC was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=2003065160
 XX
 SQ Sequence 143 AA;
 Query Match 88.9%; Score 426.5; DB 6; Length 143;
 Best Local Similarity 90.9%; Pred. No. 5e-44; 7; Indels 1; Gaps 1;
 Matches 80; Conservative 0; Mismatches 7;
 QY 1 AGKCDVAFKGFSPDCLTKLGDG-MANYPQGLDDKNTIKTCVYEDFHSCTVATLTCQEG 59
 Db 28 AGKCDVAFKGFSPDCLTKLGDGXXXXPAAWMDKNTIKTCVYEDFHSCTVATLTCQEG 87
 QY 60 AKDMDKLRKESKNTNIGSLFELCGSG 87
 Db 88 AKDMDKLRKESKNTNIGSLFELCGSG 115
 AC ABO26986;
 AC ABO26986;
 DT 10-SEP-2003 (first entry)
 DT
 DE Protein associated with novel secreted protein gene 192 #6.
 DE
 XX Secreted protein; precerebellin-like protein; sepsis; acne; psoriasis;

```

PR 05-SEP-1997; 97US-0057760P.
PR 05-SEP-1997; 97US-0057762P.
PR 05-SEP-1997; 97US-0057762B.
PR 05-SEP-1997; 97US-0057763B.
PR 05-SEP-1997; 97US-0057764P.
PR 05-SEP-1997; 97US-0057765P.
PR 05-SEP-1997; 97US-0057769P.
PR 05-SEP-1997; 97US-0057770C.
PR 05-SEP-1997; 97US-0057771P.
PR 05-SEP-1997; 97US-0057774P.
PR 05-SEP-1997; 97US-0057775B.
PR 05-SEP-1997; 97US-0057775P.
PR 05-SEP-1997; 97US-0057777P.
PR 05-SEP-1997; 97US-0057778P.
PR 16-DEC-1997; 97US-0057923B.
PR 04-JUN-1998; 98WC-US011442.
PR 15-JUL-1998; 98US-00592921P.
PR 30-JUL-1998; 98US-0094657P.

XX
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
PI Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
PI Florence K, Laffleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR;
PI Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
PI Carter KC;
XX
XX WPI; 2003-511926/48.
XX
XX
XX New precerebellin-like protein, useful for diagnosing or treating
XX neurodegenerative and behavioral disorders, immune disorders, liver
XX disorders, and cancer.
XX
XX
XX Disclosure; Col 213; 156pp; English.
XX
XX
XX The invention relates to an isolated protein comprising amino acid
XX residues 33-205 or 1-205 of a novel human secreted protein appearing as
XX CC ABO2652. The protein is encoded by one of 238 disclosed cDNA sequences
XX encoding 238 secreted proteins. ABO26252 is a precerebellin-like protein.
XX Also included are a composition comprising the protein and a carrier and
XX an isolated protein produced by expressing the protein cited above by a
XX cell, and recovering the protein. The proteins are useful for diagnosing
XX or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's
XX disease, Parkinson's disease, Huntington's disease, schizophrenia, mania,
XX dementia, paranoia, psychoses or autism), immune disorders (e.g.
XX CC infection, inflammation, allergy), liver disorders (e.g. hepatoblastoma,
XX CC jaundice, hepatitis), immunological disorders (e.g. AIDS, leukaemia,
XX CC rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present
XX CC sequence is a protein associated with one of the 238 disclosed novel
XX CC secreted proteins
XX
XX
XX Sequence 143 AA;
XX
XX
XX Query Match 88.9%; Score 426.5; DB 7; Length 143;
XX Best Local Similarity 90.9%; Pred. No. 5e-44;
XX Matches 80; Conservative 0; Mismatches 7; Indels 1; Gaps 1.
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XX 1 AGKCAVAFKGFSDCLTKLGDSS-MANYFQGGDDPTNKTCTVWEDPHFSTVATLDCQEG 59
XX 28 AGKCAVAFKGFSDCLTKLGDSSXXXXXPAAMDXTNKTCTVWEDPHFSTVATLDCQEG 87
XX
XX 60 AADYMDKLRKESKNTLNIGSLFELCGSG 87
XX
XX 88 AADYMDKLRKESKNTLNIGSLFELCGSG 115
XX

```

Tue Dec 21 15:50:46 2004

us-10-670-911a-1.rapb

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:18:36 ; Search time 144 Seconds
(without alignments)
216.192 Million cell updates/sec

Title: US-10-670-911a-1

Perfect score: 480
Sequence: 1 AGKCDVAFKGFSDCLKLGD.....RKSKNLNTQGSIFELCGSG 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	100.0	87	US-10-670-911a-1	Sequence 1, Appli
2	426.5	88.9	143	US-09-933-767-1202	Sequence 1202, Ap
3	426.5	88.9	143	US-10-004-860-1202	Sequence 1202, Ap
4	426.5	88.9	143	US-10-023-282-1201	Sequence 1201, Ap
5	327	68.1	90	US-09-933-767-1201	Sequence 1201, Ap
6	327	68.1	90	US-10-004-860-1201	Sequence 1201, Ap
7	327	68.1	90	US-10-023-282-1201	Sequence 1201, Ap
8	179.5	37.4	165	US-10-001-054-44	Sequence 44, Appl
9	179.5	37.4	165	US-10-227-884-230	Sequence 230, App
10	179.5	37.4	165	US-10-230-163-230	Sequence 230, App
11	179.5	37.4	165	US-10-230-338-230	Sequence 230, App
12	179.5	37.4	165	US-10-218-631-230	Sequence 230, App
13	179.5	37.4	165	US-10-230-414-230	Sequence 230, App

14	179.5	37.4	165	US-10-232-224-230	Sequence 230, App
15	179.5	37.4	165	US-10-216-159A-230	Sequence 230, App
16	179.5	37.4	165	US-10-218-849-230	Sequence 230, App
17	179.5	37.4	165	US-10-227-873-230	Sequence 230, App
18	179.5	37.4	165	US-10-227-883-230	Sequence 230, App
19	179.5	37.4	165	US-10-219-076-230	Sequence 230, App
20	179.5	37.4	165	US-10-230-434-230	Sequence 230, App
21	179.5	37.4	165	US-10-219-003-230	Sequence 230, App
22	179.5	37.4	165	US-10-219-464-230	Sequence 230, App
23	179.5	37.4	165	US-10-219-466-230	Sequence 230, App
24	179.5	37.4	165	US-10-219-479-230	Sequence 230, App
25	179.5	37.4	165	US-10-219-481-230	Sequence 230, App
26	179.5	37.4	165	US-10-230-260-230	Sequence 230, App
27	179.5	37.4	165	US-10-232-331-230	Sequence 230, App
28	179.5	37.4	165	US-10-232-333-230	Sequence 230, App
29	179.5	37.4	165	US-10-219-536-230	Sequence 230, App
30	179.5	37.4	165	US-10-216-165-230	Sequence 230, App
31	179.5	37.4	165	US-10-218-956-230	Sequence 230, App
32	179.5	37.4	165	US-10-219-468-230	Sequence 230, App
33	179.5	37.4	165	US-10-219-478-230	Sequence 230, App
34	179.5	37.4	165	US-10-219-524-230	Sequence 230, App
35	179.5	37.4	165	US-10-219-528-230	Sequence 230, App
36	179.5	37.4	165	US-10-227-880-230	Sequence 230, App
37	179.5	37.4	165	US-10-227-881-230	Sequence 230, App
38	179.5	37.4	165	US-10-227-882-230	Sequence 230, App
39	179.5	37.4	165	US-10-227-883-230	Sequence 230, App
40	179.5	37.4	165	US-10-227-884-230	Sequence 230, App
41	179.5	37.4	165	US-10-227-885-230	Sequence 230, App
42	179.5	37.4	165	US-10-227-886-230	Sequence 230, App
43	179.5	37.4	165	US-10-227-887-230	Sequence 230, App
44	179.5	37.4	165	US-10-227-888-230	Sequence 230, App
45	179.5	37.4	165	US-10-227-889-230	Sequence 230, App

ALIGNMENTS

RESULT 1
US-10-670-911a-1
; Sequence 1, Application US/10670911A
; Publication No. US20040176291A1
; GENERAL INFORMATION:
; APPLICANT: Mediva, Eliy
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SOLUBLE CPG
; FILE REFERENCE: 01997/547002
; CURRENT APPLICATION NUMBER: US/10/670,911A
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/413,238
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-670-911a-1

Query Match 100.0%; Score 480; DB 16; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.1e-48;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGKCDVAFKGFSDCLKLGDGSMANYPOGLDKNIKTVCTYMEDEFSCVTALTDOEGA 60
DB 1 AGKCDVAFKGFSDCLKLGDGSMANYPOGLDKNIKTVCTYMEDEFSCVTALTDOEGA 60
QY 61 KDWMDKLRKSKNLNTQGSIFELCGSG 87
DB 61 KDWMDKLRKSKNLNTQGSIFELCGSG 87

RESULT 2
US-09-933-767-1202

Sequence 1202, Application US/09933767
Publication No. US20030181692A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P2
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: PCT/US01/05614
PRIOR FILING DATE: 2001-02-21
PRIOR APPLICATION NUMBER: 60/184,835
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/193,170
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 09/205,258
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: PCT/US96/11422
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/048,885
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,375
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,881
PRIOR FILING DATE: 1997-06-06
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PRIOR APPLICATION NUMBER: 60/070,923
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,159
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PRIOR APPLICATION NUMBER: 60/073,165
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,164
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/085,925
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,921
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,923
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/094,557
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1245
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1202
LENGTH: 143
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ORGANISM: Homo sapiens
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LOCATION: (49)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (50)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (51)
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NAME/KEY: SITE
LOCATION: (52)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (53)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-933-767-1202
Query Match 88.9%; Score 426.5; DB 10; Length 143;
Best Local Similarity 90.9%; Pred. No. 48-42;
Matches 80; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:13:37 ; Search time 16 Seconds
(without alignments)
523.179 Million cell updates/sec

Title: US-10-670-911A-1

Perfect score: 480

Sequence: 1 AKKCDVAFKGFSDCLKLGD.....RKESKNINQSLFELCGSG 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	480	100.0	142 2 JCG305	neuritin precursor
2	76.5	15.9	2241 2 T20971	hypothetical prote
3	76.5	15.9	2261 2 T20978	hypothetical prote
4	71.5	14.9	195 2 H88996	protein C1787.4 [1
5	71.5	14.9	2269 2 T28677	thoptry protein -
6	71.5	14.8	199 2 T28981	hypothetical prote
7	71.5	14.8	340 2 B84019	hypothetical prote
8	70	14.6	609 2 E81500	conserved hypochet
9	70	14.6	609 2 H72038	ce651 hypothetical
10	69	14.6	609 2 H86584	ce651 hypothetical
11	69	14.4	290 2 AH1681	5'-3' exonuclease
12	69	14.4	305 2 JCS844	chitinase (EC 3.2.
13	68	14.2	644 1 M1WL58	E1 protein - human
14	67	14.0	442 2 T01731	hypothetical prote
15	66	13.8	429 2 E84952	threonine synthase
16	66	13.6	201 2 F85071	hypothetical prote
17	65.5	13.6	201 2 F88990	protein C36C5.14 [
18	65	13.5	184 2 C88104	protein M10G11.1 [
19	65	13.5	322 2 T20423	hypothetical prote
20	65	13.5	433 2 T25946	hypothetical prote
21	65	13.5	483 2 T18720	hypothetical prote
22	64.5	13.4	231 2 D69225	probable membrane
23	64.5	13.3	751 2 H90410	iton-sulfur protei
24	64	13.3	256 2 G96692	hypothetical prote
25	64	13.3	1016 2 T49686	related to PEP5 pr
26	63.5	13.2	788 2 T25061	hypothetical prote
27	63	13.1	1792 2 T08878	superoxide dismut
28	63	13.1	2718 2 A23475	G surface protein
29	62.5	13.0	211 2 T01194	hypothetical prote

30	62.5	13.0	1127 2 T30334	AND-1 protein - AF
31	62.5	13.0	1863 2 G82875	hypothetical prote
32	62.5	13.0	2098 2 T18357	protein CTRP - mal
33	62	12.9	1179 2 T04584	IV resistance pro
34	62	12.9	1365 2 T30198	alkaline phosphata
35	61.5	12.8	99 2 S21461	T-cell surface gly
36	61.5	12.8	331 2 F86633	fatty acid/phospho
37	61.5	12.8	372 1 VVVPK1	coat protein VP1 -
38	61.5	12.8	612 2 H66323	protein F14D16.17
39	61.5	12.8	701 2 S48452	probable membrane
40	61.5	12.8	1276 2 S75801	probable phytochro
41	61	12.7	430 2 D64151	hypothetical prote
42	61	12.7	467 2 A81590	chromosomal repli
43	61	12.7	533 1 S75536	NADH2 dehydrogenas
44	61	12.7	1132 2 H82887	hypothetical prote
45	60.5	12.6	250 2 T29866	hypothetical prote

ALIGNMENTS

RESULT 1
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C/Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: JCG305
R/Naevae, G.S.; Ramakrishnan, M.; Kramer, R.; Heyroni, D.; Clerti, Y.; Theill, L.E.
Proc. Natl. Acad. Sci. U.S.A. 94, 2648-2653, 1997
A/Title: Neuritin: A gene induced by neural activity and neurotrophins that promotes ne
A/Reference number: JCG305; MUID:97226008; PMID:9122250
A/Accession: JCG305
A/Molecule type: mRNA
A/Residues: 1-142 <NAB>
A/Cross-references: UNIPROT:008957; GB:U88950
C/Comment: This protein promotes neurite outgrowth and arborization in primary embryoni
C/Superfamily: rat neuritin
C/Keywords: blocked carboxyl end; disulfide bond; glycoprotein; lipoprotein; phosphatid
F.1-27/Domain: signal sequence #status predicted <SIG>
F.1-28-115/Product: neuritin #status predicted <NAB>
F.116-142/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F.115/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature for
F.115/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature for

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Best Local Similarity 100.0%; Score 480; DB 2; Length 142;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AKKCDVAFKGFSDCLKLGDSEMANYPQGLDKNIKTVCTYWEFPHSCVTATLTDCEGA	60
DB	28	AKKCDVAFKGFSDCLKLGDSEMANYPQGLDKNIKTVCTYWEFPHSCVTATLTDCEGA	87
QY	61	KQWMDKLRKESKNINQSLFELCGSG	87
DB	88	KQWMDKLRKESKNINQSLFELCGSG	114

RESULT 2

T20971
hypothetical protein F15D3.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T20971

R/White, S.
submitted to the EMBL Data Library, October 1996

A/Reference number: Z19353

A/Accession: T20971

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2241 <WIL>

A/Cross-references: EMBL:Z81063; PIDN:CAR02951.1; GSPDB:GN00019; CESP:F15D3.1

C/Genetics:
A/Genes: CESP:F15D3.1

A:Map position: 1
 A:Interons: 24/1; 130/3; 172/2; 194/2; 206/1; 235/3; 297/3; 438/2; 497/3; 601/2; 737/3; 866/3; 2019/3; 2044/3

Query Match 15.9%; Score 76.5; DB 2; Length 2241;
 Best Local Similarity 31.0%; Pred. No. 7.3;
 Matches 22; Conservative 10; Mismatches 26; Indels 13; Gaps 2;

9 KGFSDCLLKLDGSMANYPQGLDPTNKTCTWEDPHSC-----TWTALTDCEGAKDM 63
 DB 1309 KGFEEKLEKVTITLSNVEMGLDPTTGI-----DSECGALMEVRLVRLMDQAGK 1360

64 WDKLRKESKYL 74
 DB 1361 WKDLAENREQ 1371

RESULT 3

hypothetical protein F15D3.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20978

R:Name: S.

Submitted to the EMBL Data Library, October 1996

A:Reference number: Z19353

A:Accession: T20978

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2261 <MIL>

A:Cross-references: EMBL:Z81063; PIDN:CA802958.1; GSPDB:GN00019; CESP:F15D3.9

A:Experimental source: clone F15D3

A:Genetics:

A:Gene: CESP:F15D3.9

A:Map position: 1

A:Interons: 24/1; 130/3; 172/2; 211/1; 240/3; 302/3; 443/2; 502/3; 606/2; 742/3; 828/2; 904/3

Query Match 15.9%; Score 76.5; DB 2; Length 2261;
 Best Local Similarity 31.0%; Pred. No. 7.3; 26; Indels 13; Gaps 2;

Matches 22; Conservative 10; Mismatches 26; Indels 13; Gaps 2;

9 KGFSDCLLKLDGSMANYPQGLDPTNKTCTWEDPHSC-----TWTALTDCEGAKDM 63

DB 1289 KGFEEKLEKVTITLSNVEMGLDPTTGI-----DSECGALMEVRLVRLMDQAGK 1340

64 WDKLRKESKYL 74

DB 1341 WKDLAENREQ 1351

RESULT 4

Protein C17B7.4 (imported) - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: H88996

R:Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MIMD:95099613; PMID:9551516

A:Author: See websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: H88996

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-195 <STO>

A:Cross-references: UNIPROT:O45156; GB:chr_V; PIDN:AAC04398.1; PID:G2911826; GSPDB:GN000

C:Genetics:

A:Gene: C17B7.4

A:Map position: 5

C:Superfamily: Caenorhabditis elegans hypothetical protein C01B7.7

Query Match 14.9%; Score 71.5; DB 2; Length 195;
 Best Local Similarity 31.0%; Pred. No. 1.8;
 Matches 27; Conservative 10; Mismatches 37; Indels 13; Gaps 5;

5 DAVKGFSDCLLKLDGSMANYPQGLDPTNKTCTWEDPHSCVTTALTDCEG 59
 DB 37 ELTRKFFVCLYRGDFMTXK-YFLDVKSPNSNKRFTSLSMAD---CTES--FEQNN 90

60 AK--DMWDKLRKESKNTNIOGSLFELC 84
 DB 91 KEPTDSKXVRESCELTNFGTDPTTC 117

RESULT 5

rhodry protein - Plasmodium yoelii

C:Species: Plasmodium yoelii

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T28677; C45521

R:Keen, J.; Sinha, K.; Brown, K.; Holder, A.

Mol. Biochem. Parasitol. 65, 171-177, 1994

A:Title: A gene coding for a high molecular mass rhodry protein of Plasmodium yoelii

A:Reference number: Z20508; MIMD:95021522; PMID:7935623

A:Accession: T28677

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2269 <KXB>

A:Cross-references: UNIPROT:Q26223; EMBL:L27838; NID:9457145; PID:9457146; PIDN:AAC01

R:Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.

Mol. Biochem. Parasitol. 42, 241-246, 1990

A:Title: Identification of the gene for a Plasmodium yoelii rhodry protein. Multigene

A:Reference number: A45521; MIMD:91101660; PMID:2270106

A:Accession: C45521

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 2131-2269 <KE2>

A:Cross-references: GB:M34283

Query Match 14.9%; Score 71.5; DB 2; Length 2269;
 Best Local Similarity 22.8%; Pred. No. 26;

Matches 23; Conservative 21; Mismatches 32; Indels 25; Gaps 3;

8 KGFSDCLLKLDGSMANYPQGLDPTNKTCTWEDPHSCVTTALTDCEG 50

DB 15 FKGLESMIKLXNSGLIRKTTISNQIKKLVSTYEGRGFTSLSLAKSWKTKLETI 74

51 TALTDCEGA-----KDMWDKLRKESKNTNIOGSLFEL 83

DB 75 TELTKSNETVRLKEIRELFKRYLDEARKYLEGKLEL 115

RESULT 6

hypothetical protein T28A11.16 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T28981

R:Roehlfing, T.

Submitted to the EMBL Data Library, January 1997

A:Description: The sequence of C. elegans cosmid T28A11.

A:Reference number: Z20550

A:Accession: T28981

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-199 <ROH>

A:Cross-references: UNIPROT:P91512; EMBL:U80027; PIDN:AAC48125.1; GSPDB:GN00023; GSPDB

A:Experimental source: strain Bristol N2; clone T28A11

C:Genetics:

A:Gene: CESP:T28A11.16

A:Map position: 5

A:Interons: 53/3; 183/3

C:Superfamily: Caenorhabditis elegans hypothetical protein C01B7.7